

JC08 Rec'd PCT/PTO 20 APR 2001

SEQUENCE LISTING

<110> MEIJI SEIKA KAISHA, LTD.

<120> Endoglucanase and cellulase composition containing the
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<150> JP302387/1998

<151> 1998-10-23

<160> 113

<170> PatentIn Ver. 2.0

<210> 1

<211> 328

<212> PRT

<213> Rhizopus oryzae CP96001

<220>

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<222> (-23)... (-1)

<221> mat_peptide

<222> (1)... (315)

Sub
B8

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 30 35 40
 Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys Lys Thr Thr Thr
 45 50 55
 Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr
 60 65 70
 Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala Ser Thr Pro Ser
 75 80 85
 Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala Val Ser Gly Gly
 90 95 100 105
 Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala
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 Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser
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 Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser Asn Ala Gln Ser
 140 145 150
 Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp
 155 160 165
 Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser
 170 175 180 185
 Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe

190 195 200
 Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val Gln Val Thr Asn
 205 210 215
 Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln
 220 225 230
 Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln Trp
 235 240 245
 Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser
 250 255 260 265
 Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys
 270 275 280
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<212> DNA

<213> Rhizopus oryzae CP96001

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 Cys Gly Gly Lys Asn Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser
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 acc tgt aaa gta agc aac gat tac tac tct caa tgt ctt ccc tct gga 192
 Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Ser Gly
 30 35 40
 agc agt ggc aat aaa tct tct gaa agt gct cac aag aag act acc act 240
 Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys Lys Thr Thr Thr
 45 50 55
 gct gct cac aag aag act act acc gct gct cat aaa aag act acc act 288
 Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr
 60 65 70
 gct cct gct aag aag act aca act gtt gcc aaa gct tcc acc cct tct 336
 Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala Ser Thr Pro Ser
 75 80 85
 aac tct agc tct agc tcc agc ggc aaa tat tcc gct gtc tct ggt ggt 384
 Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala Val Ser Gly Gly
 90 95 100 105
 gcc tct ggt aac ggt gtc act act cgt tat tgg gat tgc tgt aag gcc 432
 Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala
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Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp			
155	160	165	
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Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser			
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Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val Gln Val Thr Asn			
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Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln Trp			
235	240	245	
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Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser			
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gca tct gac tgc tct agt ctt cct tcc gca ctc caa gct ggt tgt aaa			912
Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys			
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Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr

285

290

295

aag gaa gtt acc tgt cct aag gaa atc acc gcc aag aca ggt tgt tca 1008

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300

305

310

aga aaa taa

1017

Arg Lys

315

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<212> PRT

<213> Rhizopus oryzae CP96001

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<222> (-23)... (-1)

<221> mat_peptide

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-15

-10

Gly Thr Glu Met Ala Ser Ala Ala Lys Cys Ser Lys Leu Tyr Gly Gln

-5

1

5

Cys Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser

10

15

20

25

Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu

30

35

40

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Ser Asn Gly Asn Lys Ser Ser Glu Cys Ser Lys Leu Tyr Gly Gln Cys
 45 50 55
 Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr
 60 65 70
 Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu Ser
 75 80 85
 Asn Gly Asn Lys Thr Ser Glu Ser Ala His Lys Thr Thr Thr Thr Thr
 90 95 100 105
 Ala Pro Ala Lys Glu Ile Thr Thr Thr Ala Lys Ala Ser Asn Ser Ser
 110 115 120
 Asn Ser Ser Gly Lys Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly Asn
 125 130 135
 Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala Ser Cys Ser Trp
 140 145 150
 Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser Cys Asn Lys Asp
 155 160 165
 Gly Val Thr Ala Leu Ser Asp Ser Asn Val Gln Ser Gly Cys Asn Gly
 170 175 180 185
 Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp Ala Val Asn Asp
 190 195 200
 Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser Gly Gly Gly Glu
 205 210 215
 Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe Thr Ser Thr Ser
 220 225 230
 Val Ala Gly Lys Lys Met Val Ile Gln Val Thr Asn Thr Gly Gly Asp
 235 240 245
 Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln Met Pro Gly Gly
 250 255 260 265
 Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Gly Ala Pro Asn

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270 275 280
 Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser Ala Ser Asp Cys
 285 290 295
 Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys Trp Arg Phe Asn
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 Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr Lys Glu Val Thr
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acc tgt aaa gta agc aac gat tac tac tct caa tgt ctt gcc cct gaa				192
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Ser Asn Gly Asn Lys Ser Ser Glu Cys Ser Lys Leu Tyr Gly Gln Cys				
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ggt ggt aag gac tgg aat ggc cct act tgt tgc gaa tct gga tcc acc				288
Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr				
	60	65	70	
tgt aaa gta agc aac gat tac tac tct caa tgt ctt gcc cct gaa agc				336
Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu Ser				
	75	80	85	
aat ggc aat aaa act tct gaa agc gct cat aaa acg act act acc act				384
Asn Gly Asn Lys Thr Ser Glu Ser Ala His Lys Thr Thr Thr Thr Thr				
	90	95	100	105
gct ccc gct aag gaa att aca act act gcc aaa gct tca aac tct tct				432
Ala Pro Ala Lys Glu Ile Thr Thr Thr Ala Lys Ala Ser Asn Ser Ser				
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aac tct agc ggc aaa tac tcc att gtc tct ggt ggt gcc tct ggt aac				480
Asn Ser Ser Gly Lys Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly Asn				
	125	130	135	
ggt gtc act act cgt tat tgg gat tgc tgt aag gcc tcc tgt agc tgg				528
Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala Ser Cys Ser Trp				
	140	145	150	
ccc ggt aag gcc aat gtc agt tct cct gtc aag tcc tgt aac aaa gat				576
Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser Cys Asn Lys Asp				
	155	160	165	
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Gly Val Thr Ala Leu Ser Asp Ser Asn Val Gln Ser Gly Cys Asn Gly
 170 175 180 185
 ggt aac agt tac atg tgt aac gac aac cag cct tgg gct gta aac gat 672
 Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp Ala Val Asn Asp
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 Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser Gly Gly Gly Glu
 205 210 215
 tct cgc tgg tgc tgt tct tgt ttc gaa ctt act ttc act tct acc tct 768
 Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe Thr Ser Thr Ser
 220 225 230
 gtt gct ggt aag aag atg gtt atc caa gtc act aac act ggt ggt gat 816
 Val Ala Gly Lys Lys Met Val Ile Gln Val Thr Asn Thr Gly Gly Asp
 235 240 245
 ctt ggc tcc tct act ggt gct cac ttt gac ttg caa atg ccc ggt ggt 864
 Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln Met Pro Gly Gly
 250 255 260 265
 ggt gtt ggt att ttc aat ggt tgc tcc aag caa tgg ggt gct ccc aat 912
 Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Gly Ala Pro Asn
 270 275 280
 gac ggt tgg ggc tgc aga tac ggt ggt att tct tct gca tct gac tgc 960
 Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser Ala Ser Asp Cys
 285 290 295
 tct agt ctt cct tcc gca ctc caa gct ggt tgt aaa tgg aga ttc aac 1008
 Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys Trp Arg Phe Asn
 300 305 310
 tgg ttc aag aac gct gat aac cca agc atg act tac aag gaa gtt acc 1056
 Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr Lys Glu Val Thr
 315 320 325

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tgt ccc aag gaa atc acc gcc aag aca ggt tgt tca aga aaa taa 1101
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<213> Rhizopus oryzae CP96001

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 Cys Gly Gly Lys Asn Trp Asp Gly Pro Thr Cys Cys Glu Ser Gly Ser
 10 15 20 25
 Thr Cys Val Asp Tyr Pro Asp Asn Pro Phe Tyr Ser Gln Cys Val Pro
 30 35 40
 Asn Glu Asn Leu Thr Ser Thr Asn Lys Ser Ser His Lys Thr Thr Thr
 45 50 55
 Thr Glu Ser Ala Lys Lys Thr Thr Thr Thr Lys Gly Ser Lys Lys Thr
 60 65 70
 Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Glu Ala Ser Lys

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75	80	85
Lys Thr Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Lys		
90	95	100 105
Lys Ala Ser Thr Ser Thr Ser Ser Ser Ser Ser Ala Ser Thr Asn		
	110	115 120
Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly Asn Gly Glu Thr Thr Arg		
	125	130 135
Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ser Trp Pro Gly Lys Ala Asp		
	140	145 150
Val Thr Ser Pro Val Gly Ser Cys Asn Lys Asp Gly Lys Thr Leu Ala		
	155	160 165
Asp Asn Asn Thr Gln Asn Gly Cys Val Gly Gly Ser Ser Tyr Thr Cys		
170	175	180 185
Asn Asp Asn Gln Pro Trp Val Val Ser Asp Asp Leu Ala Tyr Gly Phe		
	190	195 200
Ala Ala Ala Ser Ile Ser Gly Gly Ser Glu Ala Thr Trp Cys Cys Ala		
	205	210 215
Cys Phe Glu Leu Thr Phe Thr Ser Thr Ala Val Lys Gly Lys Lys Met		
	220	225 230
Val Val Gln Val Thr Asn Thr Gly Ser Asp Leu Gly Ser Asn Thr Gly		
	235	240 245
Ala His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Tyr Asn		
250	255	260 265
Gly Cys Ala Thr Gln Trp Gly Ala Pro Thr Asp Gly Trp Gly Ala Arg		
	270	275 280
Tyr Gly Gly Val Ser Ser Ala Ser Asp Cys Ser Asn Leu Pro Ser Ala		
	285	290 295
Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn Ala Asp		
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Asn Pro Thr Met Thr Tyr Lys Gln Val Thr Cys Pro Lys Ala Ile Thr

315

320

325

Ala Lys Ser Gly Cys Ser Arg Lys

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<210> 6

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<212> DNA

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Cys Gly Gly Lys Asn Trp Asp Gly Pro Thr Cys Cys Glu Ser Gly Ser	
10 15 20 25	
act tgc gtt gat tat cct gac aat cct ttc tac tcc caa tgt gtt ccc	192
Thr Cys Val Asp Tyr Pro Asp Asn Pro Phe Tyr Ser Gln Cys Val Pro	
30 35 40	
aat gaa aac ctc acc tcc act aac aaa tct tct cac aaa acc acc act	240

Asn	Glu	Asn	Leu	Thr	Ser	Thr	Asn	Lys	Ser	Ser	His	Lys	Thr	Thr	Thr	
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Thr	Glu	Ser	Ala	Lys	Lys	Thr	Thr	Thr	Thr	Lys	Gly	Ser	Lys	Lys	Thr	
60				65				70								
acc	act	act	gaa	gcc	tct	aag	aag	acc	acc	act	act	gaa	gct	tcc	aag	336
Thr	Thr	Thr	Glu	Ala	Ser	Lys	Lys	Thr	Thr	Thr	Thr	Glu	Ala	Ser	Lys	
75				80				85								
aag	acc	acc	act	act	gaa	gcc	tct	aag	aag	acc	acc	act	act	act	aag	384
Lys	Thr	Thr	Thr	Thr	Glu	Ala	Ser	Lys	Lys	Thr	Thr	Thr	Thr	Thr	Lys	
90				95				100				105				
aag	gct	tct	acc	tcc	act	tcc	tct	tcc	tct	tct	tct	gct	tct	aca	aac	432
Lys	Ala	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Ser	Ser	Ser	Ala	Ser	Thr	Asn	
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tac	tcc	gct	gtc	tct	ggt	ggt	gcc	tcc	ggt	aat	ggt	gaa	acc	act	cgc	480
Tyr	Ser	Ala	Val	Ser	Gly	Gly	Ala	Ser	Gly	Asn	Gly	Glu	Thr	Thr	Arg	
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Tyr	Trp	Asp	Cys	Cys	Lys	Pro	Ser	Cys	Ser	Trp	Pro	Gly	Lys	Ala	Asp	
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gtc	acc	tcc	ccg	gtt	ggc	tcc	tgt	aac	aag	gat	ggt	aag	act	ctt	gct	576
Val	Thr	Ser	Pro	Val	Gly	Ser	Cys	Asn	Lys	Asp	Gly	Lys	Thr	Leu	Ala	
155				160				165								
gat	aac	aac	act	caa	aac	ggc	tgt	gtt	ggt	ggt	agc	agc	tac	acc	tgt	624
Asp	Asn	Asn	Thr	Gln	Asn	Gly	Cys	Val	Gly	Gly	Ser	Ser	Tyr	Thr	Cys	
170				175				180				185				
aat	gac	aat	caa	ccg	tgg	gtt	gtt	agc	gac	gac	ctt	gcc	tac	ggt	ttc	672
Asn	Asp	Asn	Gln	Pro	Trp	Val	Val	Ser	Asp	Asp	Leu	Ala	Tyr	Gly	Phe	
190				195				200								

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 tgt ttc gaa ctc aca ttc acc tct act gcc gtc aag ggt aag aag atg 768
 Cys Phe Glu Leu Thr Phe Thr Ser Thr Ala Val Lys Gly Lys Lys Met
 220 225 230
 gtt gtt caa gta acc aac act ggt tct gac ctt ggc tct aac act ggt 816
 Val Val Gln Val Thr Asn Thr Gly Ser Asp Leu Gly Ser Asn Thr Gly
 235 240 245
 gct cac ttt gac ttg caa atg ccc ggt ggt ggt gtt ggt atc tac aat 864
 Ala His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Tyr Asn
 250 255 260 265
 ggt tgt gcc act caa tgg ggt gct ccc acc gat ggt tgg ggt gca aga 912
 Gly Cys Ala Thr Gln Trp Gly Ala Pro Thr Asp Gly Trp Gly Ala Arg
 270 275 280
 tac ggc ggt gtt tct tct gcc tct gac tgt tct aac ctt cct tct gcc 960
 Tyr Gly Gly Val Ser Ser Ala Ser Asp Cys Ser Asn Leu Pro Ser Ala
 285 290 295
 ctt caa gct ggt tgt aag tgg aga ttc ggc tgg ttc aaa aac gct gat 1008
 Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn Ala Asp
 300 305 310
 aac cca acc atg acc tac aaa caa gtt acc tgt ccc aag gct atc act 1056
 Asn Pro Thr Met Thr Tyr Lys Gln Val Thr Cys Pro Lys Ala Ile Thr
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 gcc aag tct ggc tgt tca aga aaa taa 1083
 Ala Lys Ser Gly Cys Ser Arg Lys
 330 335

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              15                      20                      25
Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro Gly
              30                      35                      40
Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr Ser
              45                      50                      55
Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr Thr
              60                      65                      70
Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser Thr
              75                      80                      85                      90
Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys Val
              95                      100                      105
Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp Asp
              110                      115                      120
Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr Gly

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125	130	135
Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala Asn		
140	145	150
Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn Asn		
155	160	165
Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Ala		
175	180	185
Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr Glu		
190	195	200
Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val Gln		
205	210	215
Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu Gln		
220	225	230
Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln Trp		
235	240	245
Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser Ser		
255	260	265
Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys		
270	275	280
Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr Phe		
285	290	295
Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys Glu		
300	305	310
Arg Lys		
315		

<210> 8

<211> 1017

<212> DNA

<213> Mucor circinelloides CP99001

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<221> sig_peptide

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agc tct tct gct gaa gct gct tct tgc agc tct gtc tat ggt caa tgt	96
Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys	
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ggt ggc att gga tgg agt gga cct acc tgt tgt gaa agt ggc tct act	144
Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr	
15 20 25	
tgc gtt gct caa gaa ggc aac aaa tac tac tct caa tgt ctt ccc gga	192
Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro Gly	
30 35 40	
tcc cac agt aac aat gct ggt aac gct agc agc acc aag aag aca tct	240
Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr Ser	
45 50 55	
acc aag aca tct act acc acc gcc aag gct act gct act gtc acc acc	288
Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr Thr	
60 65 70	
aag aca gla acc aag aca act acc aag aca act acc aag act agc act	336
Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser Thr	
75 80 85 90	

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act gcc gct gct tct act tcc acc tct tct tct gct ggt tac aag gtc 384
 Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys Val
 95 100 105
 atc tct ggc ggt aaa tct ggc agt ggt tcc aca act cgt tat tgg gat 432
 Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp Asp
 110 115 120
 tgt tgt aaa gct tct tgc agc tgg cct gga aaa gct tct gtc act ggt 480
 Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr Gly
 125 130 135
 cct gtt gac acc tgt gcc tcc aat ggt atc tct tta tta gat gcc aat 528
 Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala Asn
 140 145 150
 gct caa agt ggt tgt aac ggt ggt aat ggt ttc atg tgt aac aac aac 576
 Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn Asn
 155 160 165 170
 caa cct tgg gct gtc aat gat gag ctc gct tac ggt ttc gct gct gcc 624
 Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Ala
 175 180 185
 tct att gct ggc tcc aac gaa gct gga tgg tgt tgt ggc tgt tat gaa 672
 Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr Glu
 190 195 200
 ttg acc ttc act tct ggc gct gct tct gga aag aag atg gtt gtt caa 720
 Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val Gln
 205 210 215
 gtt acc aac acc ggt ggc gat tta ggc tct aac cac ttt gat ttg caa 768
 Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu Gln
 220 225 230
 atg ccc ggt ggt ggc gtt ggt atc ttc aat ggc tgt gct gct caa tgg 816
 Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln Trp

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235 240 245 250
 ggc gct ccc aat gat ggc tgg gga gct aga tat ggt ggt gtc agc tct 864
 Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser Ser
 255 260 265
 gtc tct gac tgt gcc tct ctt ccc tct gct ctt caa gct ggt tgt aaa 912
 Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys
 270 275 280
 tgg aga ttc aac tgg ttc aag aac tct gat aac cct acc atg acc ttc 960
 Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr Phe
 285 290 295
 aag gaa gtt acc tgt cct gct gaa tta act act cgc tca ggt tgc gaa 1008
 Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys Glu
 300 305 310
 aga aag taa 1017
 Arg Lys
 315

<210> 9

<211> 387

<212> PRT

<213> *Mucor circinelloides* CP99001

<220>

<221> sig_peptide

<222> (-22)... (-1)

<221> mat_peptide

<222> (1)... (365)

<400> 9

Met Lys Phe Thr Val Ala Ile Thr Ser Ile Ala Val Ala Leu Ala Leu

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-20	-15	-10
Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys		
-5	1	5
		10
Gly Gly Ile Gly Trp Thr Gly Pro Thr Cys Cys Asp Ala Gly Ser Thr		
15	20	25
Cys Lys Ala Gln Lys Asp Asn Lys Tyr Tyr Ser Gln Cys Ile Pro Lys		
30	35	40
Pro Lys Gly Ser Ser Ser Ser Ser Ser Cys Ser Ser Val Tyr Ser Gln		
45	50	55
Cys Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser		
60	65	70
Thr Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro		
75	80	85
		90
Gly Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr		
95	100	105
Ser Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr		
110	115	120
Thr Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser		
125	130	135
Thr Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys		
140	145	150
Val Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp		
155	160	165
		170
Asp Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr		
175	180	185
Gly Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala		
190	195	200
Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn		
205	210	215

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Asn Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala
 220 225 230
 Ala Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr
 235 240 245 250
 Glu Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val
 255 260 265
 Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu
 270 275 280
 Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln
 285 290 295
 Trp Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser
 300 305 310
 Ser Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys
 315 320 325 330
 Lys Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr
 335 340 345
 Phe Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys
 350 355 360
 Glu Arg Lys
 365

<210> 10

<211> 1164

<212> DNA

<213> Mucor circinelloides CP99001

<220>

<221> sig_peptide

<222> (1)... (66)

<221> mat_peptide

<222> (67)... (1164)

<400> 10

atg aag ttc acc gtt gct att act tca atc gct gtt gca ctc gct ctc	48
Met Lys Phe Thr Val Ala Ile Thr Ser Ile Ala Val Ala Leu Ala Leu	
-20 -15 -10	
agc tct tct gct gaa gct gct tct tgc agc tct gtc tat ggt caa tgt	96
Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys	
-5 1 5 10	
ggc ggc att ggc tgg act ggt cct aca tgt tgt gat gct gga tgc acc	144
Gly Gly Ile Gly Trp Thr Gly Pro Thr Cys Cys Asp Ala Gly Ser Thr	
15 20 25	
tgt aaa gct caa aag gat aac aaa tat tat tct caa tgt att ccc aaa	192
Cys Lys Ala Gln Lys Asp Asn Lys Tyr Tyr Ser Gln Cys Ile Pro Lys	
30 35 40	
ccc aag ggt tcc tcc tca tca tca tca tgt agt tcc gtc tat agt caa	240
Pro Lys Gly Ser Ser Ser Ser Ser Ser Cys Ser Ser Val Tyr Ser Gln	
45 50 55	
tgc ggt ggc att gga tgg agt gga cct acc tgt tgt gaa agt ggc tct	288
Cys Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser	
60 65 70	
act tgc gtt gct caa gaa ggc aac aaa tac tac tct caa tgt ctt ccc	336
Thr Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro	
75 80 85 90	
gga tcc cac agt aac aat gct ggt aac gct agc agc acc aag aag aca	384
Gly Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr	
95 100 105	
tct acc aag aca tct act acc acc gcc aag gct act gct act gtc acc	432
Ser Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr	

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110	115	120	
acc aag aca gta acc aag aca act acc aag aca act acc aag act agc			480
Thr Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser			
125	130	135	
act act gcc gct gct tct act tcc acc tct tct tct gct ggt tac aag			528
Thr Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys			
140	145	150	
gtc atc tct ggc ggt aaa tct ggc agt ggt tcc aca act cgt tat tgg			576
Val Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp			
155	160	165	170
gat tgt tgt aaa gct tct tgc agc tgg cct gga aaa gct tct gtc act			624
Asp Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr			
175	180	185	
ggt cct gtt gac acc tgt gcc tcc aat ggt atc tct tta tta gat gcc			672
Gly Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala			
190	195	200	
aat gct caa agt ggt tgt aac ggt ggt aat ggt ttc atg tgt aac aac			720
Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn			
205	210	215	
aac caa cct tgg gct gtc aat gat gag ctc gct tac ggt ttc gct gct			768
Asn Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala			
220	225	230	
gcc tct att gct ggc tcc aac gaa gct gga tgg tgt tgt ggc tgt tat			816
Ala Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr			
235	240	245	250
gaa ttg acc ttc act tct ggc gct gct tct gga aag aag atg gtt gtt			864
Glu Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val			
255	260	265	
caa gtt acc aac acc ggt ggc gat tta ggc tct aac cac ttt gat ttg			912

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Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu
 270 275 280
 caa atg ccc ggt ggt ggc gtt ggt atc ttc aat ggc tgt gct gct caa 960
 Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln
 285 290 295
 tgg ggc gct ccc aat gat ggc tgg gga gct aga tat ggt ggt gtc agc 1008
 Trp Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser
 300 305 310
 tct gtc tct gac tgt gcc tct ctt ccc tct gct ctt caa gct ggt tgt 1056
 Ser Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys
 315 320 325 330
 aaa tgg aga ttc aac tgg ttc aag aac tct gat aac cct acc atg acc 1104
 Lys Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr
 335 340 345
 ttc aag gaa gtt acc tgt cct gct gaa tta act act cgc tca ggt tgc 1152
 Phe Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys
 350 355 360
 gaa aga aag taa 1164
 Glu Arg Lys
 365

<210> 11

<211> 346

<212> PRT

<213> Phycomyces nitens CP99002

<220>

<221> sig_peptide

<222> (-19)... (-1)

<221> mat_peptide

$\langle 222 \rangle$ (1)... (327)

<400> 11

Met Lys Phe Ser Ile Ile Ala Ser Ala Leu Leu Leu Ala Ala Ser Ser
-15 -10 -5
Thr Tyr Ala Ala Glu Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys
1 5 10
Met Trp Thr Gly Pro Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly
15 20 25
Ala Glu Asn Asn Glu Trp Tyr Ser Gln Cys Ile Pro Asn Asp Gln Val
30 35 40 45
Gln Gly Asn Pro Lys Thr Thr Thr Thr Thr Thr Thr Lys Ala Ala Thr
50 55 60
Thr Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr
65 70 75
Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr Thr
80 85 90
Lys Thr Thr Thr Lys Thr Thr Thr Thr Lys Ala Ala Thr Thr Thr Ser
95 100 105
Ser Ser Asn Thr Gly Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly Asn
110 115 120 125
Gly Arg Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp
130 135 140
Asp Gly Lys Ala Ser Val Thr Lys Pro Val Leu Thr Cys Ala Lys Asp
145 150 155
Gly Val Ser Arg Leu Gly Ser Asp Val Gln Ser Gly Cys Val Gly Gly
160 165 170
Gln Ala Tyr Met Cys Asn Asp Asn Gln Pro Trp Val Val Asn Asp Asp
175 180 185

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Leu Ala Tyr Gly Phe Ala Ala Ala Ser Leu Gly Ser Ala Gly Ala Ser
 190 195 200 205
 Ala Phe Cys Cys Gly Cys Tyr Glu Leu Thr Phe Thr Asn Thr Ala Val
 210 215 220
 Ala Gly Lys Lys Phe Val Val Gln Val Thr Asn Thr Gly Asp Asp Leu
 225 230 235
 Ser Thr Asn His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Tyr
 240 245 250
 Phe Asn Gly Cys Gln Ser Gln Trp Asn Thr Asn Thr Asp Gly Trp Gly
 255 260 265
 Ala Arg Tyr Gly Gly Ile Ser Ser Ile Ser Glu Cys Asp Lys Leu Pro
 270 275 280 285
 Thr Gln Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn
 290 295 300
 Ala Asp Asn Pro Glu Val Thr Phe Lys Ala Val Thr Cys Pro Ala Glu
 305 310 315
 Ile Ile Ala Lys Thr Gly Cys Glu Arg Lys
 320 325

<210> 12

<211> 1041

<212> DNA

<213> *Phycomyces nitens* CP99002

<220>

<221> sig_peptide

<222> (1)... (57)

<221> mat_peptide

<222> (58)... (1041)

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<400> 12

atg aag ttc tcc atc atc gct tcc gcc ctt ctc ctc gct gcc agc tcc	48
Met Lys Phe Ser Ile Ile Ala Ser Ala Leu Leu Leu Ala Ala Ser Ser	
-15 -10 -5	
act tac gct gct gaa tgc agc caa ggc tat ggc cag tgt ggt ggc aag	96
Thr Tyr Ala Ala Glu Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys	
1 5 10	
atg tgg act ggt ccc acc tgc tgc acc tcc ggc ttc acc tgt gta ggt	144
Met Trp Thr Gly Pro Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly	
15 20 25	
gcc gaa aac aac gag tgg tac tct cag tgt atc ccc aac gat caa gtc	192
Ala Glu Asn Asn Glu Trp Tyr Ser Gln Cys Ile Pro Asn Asp Gln Val	
30 35 40 45	
cag ggt aac ccc aag acc acc acc acc acc acc acc aag gct gcc act	240
Gln Gly Asn Pro Lys Thr Thr Thr Thr Thr Thr Thr Lys Ala Ala Thr	
50 55 60	
acc acc aag gct cct gtc acc acc acc aag gcc acc acc acc acc acc	288
Thr Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr	
65 70 75	
acc aag gcc cct gtc acc acc acc aag gcc act act act acc acc acc	336
Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr Thr	
80 85 90	
aag acc acc acc aag acc acc acc acc aag gct gcc acc acc acc tcc	384
Lys Thr Thr Thr Lys Thr Thr Thr Thr Lys Ala Ala Thr Thr Thr Ser	
95 100 105	
tcg tcc aac act ggc tac agc ccc att tct ggt ggc ttc tct gga aac	432
Ser Ser Asn Thr Gly Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly Asn	
110 115 120 125	
ggt cgc act acc cgc tac tgg gat tgc tgc aag ccc tct tgc gcc tgg	480

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Gly Arg Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp
 130 135 140
 gac gga aag gct tct gta act aag cct gta ctc acc tgt gcc aag gat 528
 Asp Gly Lys Ala Ser Val Thr Lys Pro Val Leu Thr Cys Ala Lys Asp
 145 150 155
 ggt gtc agc cgt ctc ggt tcc gat gtc cag agc ggt tgc gtc ggc ggc 576
 Gly Val Ser Arg Leu Gly Ser Asp Val Gln Ser Gly Cys Val Gly Gly
 160 165 170
 cag gcc tac atg tgc aat gac aac cag ccc tgg gtt gtc aat gac gac 624
 Gln Ala Tyr Met Cys Asn Asp Asn Gln Pro Trp Val Val Asn Asp Asp
 175 180 185
 ctt gcc tac ggt ttc gct gct gcc agt ctc ggt agc gcc ggt gcc tct 672
 Leu Ala Tyr Gly Phe Ala Ala Ala Ser Leu Gly Ser Ala Gly Ala Ser
 190 195 200 205
 gca ttc tgc tgc ggc tgt tac gag ctt acc ttc acc aac act gct gtc 720
 Ala Phe Cys Cys Gly Cys Tyr Glu Leu Thr Phe Thr Asn Thr Ala Val
 210 215 220
 gct ggc aag aag ttt gtc gtc cag gtc acc aac acc ggt gat gat ctc 768
 Ala Gly Lys Lys Phe Val Val Gln Val Thr Asn Thr Gly Asp Asp Leu
 225 230 235
 agc acc aac cac ttt gat ttg cag atg ccc ggc ggt ggt gtc ggc tac 816
 Ser Thr Asn His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Tyr
 240 245 250
 ttc aac ggc tgc cag tcc cag tgg aac acc aac acc gat ggc tgg ggt 864
 Phe Asn Gly Cys Gln Ser Gln Trp Asn Thr Asn Thr Asp Gly Trp Gly
 255 260 265
 gct cgc tal ggc ggt att agc tct att tca gag tgc gac aag ctt cct 912
 Ala Arg Tyr Gly Gly Ile Ser Ser Ile Ser Glu Cys Asp Lys Leu Pro
 270 275 280 285

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acc cag ttg cag gct ggt tgc aag tgg aga ttc gga tgg ttc aag aac 960
 Thr Gln Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn
 290 295 300
 gct gac aac cca gag gtc acc ttc aag gct gtt act tgc cct gcc gag 1008
 Ala Asp Asn Pro Glu Val Thr Phe Lys Ala Val Thr Cys Pro Ala Glu
 305 310 315
 atc att gcc aag act ggt tgc gag cgc aag taa 1041
 Ile Ile Ala Lys Thr Gly Cys Glu Arg Lys
 320 325

<210> 13

<211> 1043

<212> DNA

<213> Artificial Sequence

<220>

<221> sig_peptide

<222> (16)... (84)

<221> mat_peptide

<222> (84)... (1043)

<400> 13

ggatccctggg acaag atg aag ttc atc act atc gcc tcc tcc gcc ctc ctt 51
 Met Lys Phe Ile Thr Ile Ala Ser Ser Ala Leu Leu

-20

-15

gcc ctc gcc ctt ggc act gag atg gcc tcc gcc gct gag tgc tcc aag 99
 Ala Leu Ala Leu Gly Thr Glu Met Ala Ser Ala Ala Glu Cys Ser Lys

-10

-5

1

5

ctc tac gga cag tgc ggc gga aag aac tgg aac ggc ccc acc tgc tgc 147
 Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn Gly Pro Thr Cys Cys

10	15	20	
gag agc ggc tgc acc tgc aag gtc tgc aat gac tac tac agc cag tgc			195
Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys			
25	30	35	
ctg ccg agc ggc tcc tgc gga aac aag tgc agc gag tgc gcc cac aag			243
Leu Pro Ser Gly Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys			
40	45	50	
aag acc acg acc gct gcc cac aag aag acc acg acc gcc gct cac aag			291
Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys			
55	60	65	
aag act acg acc gct ccc gcc aag aag acc acg acc gtc gcc aag gct			339
Lys Thr Thr Thr Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala			
70	75	80	85
tcg act ccg tcc aac tgc agc agc tgc tct tgc gga aag tac agc gct			387
Ser Thr Pro Ser Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala			
90	95	100	
gtc agc ggt ggc gct agc ggc aac ggc gtc act acc cgc tac tgg gac			435
Val Ser Gly Gly Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp			
105	110	115	
tgc tgc aag gct tgc tgc tgc tgg ccc ggc aag gct aac gtc agc tgc			483
Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser			
120	125	130	
cct gtc aag tcc tgc aac aag gac ggc gtc acc gct ctt agc gac tcc			531
Pro Val Lys Ser Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser			
135	140	145	
aac gcc cag tcc ggc tgc aac ggc ggc aac tcc tac atg tgc aac gac			579
Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp			
150	155	160	165
aac cag cca tgg gct gtc aac gac aac ctt gct tac ggt ttc gct gcc			627

Asn Gln Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala
 170 175 180
 gct gcc att agc ggc ggt ggc gag agc cgc tgg tgc tgc tcc tgc ttc 675
 Ala Ala Ile Ser Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe
 185 190 195
 gag ctc acc ttc acc tcc acc agc gtt gct ggc aag aag atg gtc gtc 723
 Glu Leu Thr Phe Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val
 200 205 210
 cag gtc acc aac act ggc ggt gac ctt ggc agc tgc acc ggt gcc cac 771
 Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His
 215 220 225
 ttc gat ctc cag atg ccc ggc ggc ggc gtc ggc atc ttc aac gga tgc 819
 Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys
 230 235 240 245
 tgc tcc cag tgg ggc gct ccc aac gac ggc tgg ggc tgc cgc tac ggc 867
 Ser Ser Gln Trp Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly
 250 255 260
 ggc atc agc tcc gcc agc gac tgc tgc tcc ctc ccc agc gcc ctc cag 915
 Gly Ile Ser Ser Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln
 265 270 275
 gcc ggc tgc aag tgg cgc ttc aac tgg ttc aag aac gcc gac aac ccg 963
 Ala Gly Cys Lys Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro
 280 285 290
 tcc atg acc tac aag gag gtc acc tgc ccc aag gag atc acc gct aag 1011
 Ser Met Thr Tyr Lys Glu Val Thr Cys Pro Lys Glu Ile Thr Ala Lys
 295 300 305
 acc gga tgc tgc cgc aag taa acgcagg atcc 1043
 Thr Gly Cys Ser Arg Lys
 310 315

<210> 14

<211> 40

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 14

Ala	Glu	Cys	Ser	Lys	Leu	Tyr	Gly	Gln	Cys	Gly	Gly	Lys	Asn	Trp	Asn
1				5				10				15			
Gly	Pro	Thr	Cys	Cys	Glu	Ser	Gly	Ser	Thr	Cys	Lys	Val	Ser	Asn	Asp
			20					25					30		
Tyr	Tyr	Ser	Gln	Cys	Leu	Pro	Ser								
		35					40								

<210> 15

<211> 22

<212> PRT

<213> *Mucor circinelloides* CP99001

<400> 15

Ala	Ser	Cys	Ser	Ser	Val	Tyr	Gly	Gln	Cys	Gly	Gly	Ile	Gly	Trp	Ser
1				5				10				15			
Gly	Pro	Thr	Cys	Cys	Glu										
					20										

<210> 16

<211> 23

<212> PRT

<213> *Phycomyces nitens* CP99002

<400> 16

Ala Glu Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys Met Trp Thr
 1 5 10 15
 Gly Pro Thr Cys Cys Thr Ser
 20

<210> 17

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
 sequence

<400> 17

Xaa Xaa Xaa Xaa Xaa Xaa Gln Cys Gly Gly Xaa Xaa Xaa Xaa Gly Xaa
 1 5 10 15
 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn
 20 25 30
 Xaa Xaa Tyr Xaa Gln Cys Xaa
 35

<210> 18

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 18

Xaa Xaa Xaa Xaa Xaa Xaa Gln Cys Gly Gly Xaa Xaa Xaa Xaa Gly Xaa
1 5 10 15
Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn
20 25 30
Xaa Xaa Tyr Xaa Gln Cys Xaa
35

<210> 19

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 19

Cys Ser Xaa Xaa Tyr Xaa Gln Cys Gly Gly Xaa Xaa Trp Xaa Gly Pro
1 5 10 15
Thr Cys Cys Xaa Xaa Gly Xaa Thr Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa
20 25 30
Xaa Tyr Ser Gln Cys Xaa
35

<210> 20

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 20

Cys	Ser	Xaa	Xaa	Tyr	Xaa	Gln	Cys	Gly	Gly	Xaa	Xaa	Trp	Xaa	Gly	Pro
1				5				10					15		
Thr	Cys	Cys	Xaa	Xaa	Gly	Xaa	Thr	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa
			20					25					30		
Xaa	Tyr	Ser	Gln	Cys	Xaa										
			35												

<210> 21

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 21

Cys	Ser	Lys	Xaa	Tyr	Xaa	Gln	Cys	Gly	Gly	Lys	Xaa	Trp	Xaa	Gly	Pro
1				5				10					15		

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Thr Cys Cys Glu Ser Gly Ser Thr Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa
 20 25 30

Xaa Tyr Ser Gln Cys Xaa
 35

<210> 22

<211> 36

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 22

Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn Gly Pro
 1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr
 20 25 30

Ser Gln Cys Leu
 35

<210> 23

<211> 36

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 23

Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asp Trp Asn Gly Pro
 1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr
 20 25 30

Ser Gln Cys Leu

35

<210> 24

<211> 38

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 24

Cys Ser Lys Ala Tyr Tyr Gln Cys Gly Gly Lys Asn Trp Asp Gly Pro

1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Val Asp Tyr Pro Asp Asn Pro

20 25 30

Phe Tyr Ser Gln Cys Val

35

<210> 25

<211> 38

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<400> 25

Cys Ser Ser Val Tyr Xaa Gln Cys Gly Gly Ile Gly Trp Xaa Gly Pro

1 5 10 15

Thr Cys Cys Xaa Xaa Gly Ser Thr Cys Xaa Ala Gln Xaa Xaa Asn Lys

20 25 30

35

<213> *Mucor circinelloides* CP99001

15

30

35

<213> *Mucor circinelloides* CP99001

15

30

35

<210> 28

<211> 38

<212> PRT

<213> *Phycomyces nitens* CP99002

<400> 28

Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys Met Trp Thr Gly Pro

1 5 10 15

Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly Ala Glu Asn Asn Glu

20 25 30

Trp Tyr Ser Gln Cys Ile

35

<210> 29

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (linker)

<400> 29

Xaa Thr Arg Tyr Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa

1 5 10

<210> 30

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (linker)

<400> 30

Tyr	Xaa	Xaa	Xaa	Ser	Gly	Gly	Xaa	Ser	Gly
1				5					10

<210> 31

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (linker)

<400> 31

Tyr	Xaa	Xaa	Xaa	Xaa	Gly	Gly	Xaa	Xaa	Gly
1				5					10

<210> 32

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (linker)

<400> 32

Tyr Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Gly
1 5 10

<210> 33

<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 33

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly
1 5 10

<210> 34

<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 34

Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly
1 5 10

<210> 35

<211> 10

<212> PRT

<213> *Mucor circinelloides* CP99001

<400> 35

Tyr Lys Val Ile Ser Gly Gly Lys Ser Gly

1 5 10

<210> 36

<211> 10

<212> PRT

<213> *Phycomyces nitens* CP99002

<400> 36

Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly

1 5 10

<210> 37

<211> 26

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 37

Ala Lys Ala Ser Thr Pro Ser Asn Ser Ser Ser Ser Ser Ser Gly Lys

1 5 10 15

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly

20 25

<210> 38

<211> 10

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 38

Asn Ala Asp Asn Pro Ser Met Thr Tyr Lys

1 5 10

<210> 39

<211> 10

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 39

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly

1 5 10

<210> 40

<211> 17

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 40

Ser Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys

1 5 10 15

Lys

<210> 41

<211> 18

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 41

Tyr Gly Gly Ile Ser Ser Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala

1

5

10

15

Leu Gln

<210> 42

<211> 6

<212> PRT

<213> *Rhizopus oryzae* CP96001

<400> 42

Arg Phe Asn Trp Phe Lys

1

5

<210> 43

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 43

aaraaytgga ayggncnac

20

<210> 44

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 44

tttaaccart traancg

17

<210> 45

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 45

tttaaccart traayct

17

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 46

caatgtcttc cctctggaag cag

23

<210> 47

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 47

tgcccttagt gacagcaatg ccc

23

<210> 48

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 48

cttccttccg cactccaagc tgg

23

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 49

ccagcttggga gtgcggaagg aag

23

<210> 50

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 50

tcactaaggg cagtgacacc atc

23

<210> 51

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 51

cagaggggaag acattgagag tag

23

<210> 52

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 52

acaacattat ttcttcaaac atg

23

<210> 53

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 53

aaatgccgca tcaagtttta ttg

23

<210> 54

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 54

ttcacttcta cctctgttgc tgg

23

<210> 55

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 55

gtaataaact tcatagatct atgtaaaaag aatg

34

<210> 56

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 56

ggatgagtaa aaaagatcct atttcttga ac

32

<210> 57

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 57

cactttcaga agctttattg ccac

24

<210> 58

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 58

gagctagagc cagagttaga ag

22

<210> 59

<211> 22

<212> DNA

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<220>

<223> Description of Artificial Sequence:primer

<400> 59

gagaacigac atcggcctta cc

22

<210> 60

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 60

acaacattat ttcttcgaat atg

23

<210> 61

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 61

tttagcagca gaggccattt cag

23

<210> 62

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 62

ttttctatcc tgatacagag atg

23

<210> 63

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 63

gcgcataaa aacgactact acc

23

<210> 64

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 64

tgcccttagt gacagcaatg tcc

23

<210> 65

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 65

caagaaaata agatctttta tactcctact

30

<210> 66

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 66

aacggcaata aggcctctga atgtagc

27

<210> 67

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 67

gaaagcaatg gccagaaaac ttctgaaag

29

<210> 68

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 68

gcttcaaact ctctagactc tagcggc

27

<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 69

cggtaaggcc gacgtcagtt ctcc

24

<210> 70

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 70

tacaggagcc aacaggggag gtg

23

<210> 71

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 71

ttcacagcag gtaggtccat tcc

23

<210> 72

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 72

cctacggttt cgccgctgct tcc

23

<210> 73

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 73

tagataccaa caccaccacc ggg

23

<210> 74

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 74

tgaagttcct taccattgcc tcc

23

<210> 75

<211> 23

<212> DNA

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<220>

<223> Description of Artificial Sequence:primer

<400> 75

tggtgaaacc actcgctact ggg

23

<210> 76

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 76

ttctgcctct gactgttcta acc

23

<210> 77

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 77

aatagagtta cttatatacga tag

23

<210> 78

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 78

caccaccaga gacagcggag tag

23

<210> 79

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 79

lgcgttgatt atcctgacaa tcc

23

<210> 80

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 80

gcggatccat gaagttcctt accattgcc

29

<210> 81

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 81

gcggatcctt attttcttga acagccaga

29

<210> 82

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 82

gtggagg!ga gatcttcatt gggaac

26

<210> 83

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 83

cagcggagta cttttagtaa gcag

24

<210> 84

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 84

gggagatcctt gggacaagat gaagtttatt actattg

37

<210> 85

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 85

ggcacaacaa gtcgtgcgg atcctgggac aagatggcca agtctctcct tac

53

<210> 86

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 86

gggggatcct gggacaagat gaagttaac actatgcct cctccgccct cctlgccctc 60
gcccttggca ctgagatggc ctccgccgt gagtgctcca agctctacgg ccagtgcggc 120
ggaaagaact gg 132

<210> 87

<211> 136

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 87

ggccgactcg ctgacttgt ttcccagga gccgctcggc aggcactggc tgiagtagtc 60
attcgagacc ttgcaggctg agccgctctc gcagcaggctg gggccgttcc agttctttcc 120
gccgcactgg ccgtag 136

<210> 88

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 88

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gggctcgagt tggacggagt cgaagccttg gcgacggtcg tggctctctt ggcgggagcg 60
gtcgtagtct tcttgtgagc ggcggtcgtg gtcttcttgt ggcagcggg cgtggctctc 120
ttgtgggccg actcgctcga ctgtttccc                                150
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<210> 89

<211> 158

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 89

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ggaaacaagi cgagcgagtc ggcccacaag aagaccacga ccgctgcca caagaagacc 60
acgaccgccg ctcaacaaga gactacgacc gctcccgcca agaagaccac gaccgtcgcc 120
aaggcttcga ctccgtccaa ctcgagcagc tcgtcttc                                158
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<210> 90

<211> 160

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 90

gtccttgttg caggacttga caggcgagct gacgttagcc ttgccggggc acgagcacga 60
agccttgcag cagtcccagt agcgggtagt gacgccgttg ccgctagcgc caccgctgac 120
agcgctgtac ttcccgagg acgagctgct cgagttggac 160

<210> 91

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 91

agcccatggc tggttgtcgt tgcacatgta ggagttgccg ccgttgcagc cggactgggc 60
gttggagtcg ctaagagcgg tgacgccgtc cttgttgcag gacttgacag gcgagctgac 120

<210> 92

<211> 118

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 92

ggtgagctcg aagcaggagc agcaccagcg gctctcgcca ccgccgctaa tggcagcggc 60

agcgaaaccg taagcaaggi tgcgttgac agcccatggc tggitgtcgt tgcacatg 118

<210> 93

<211> 154

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 93

gtgcccacit cgatctccag atgcccggcg gcggcgtcgg catcttcaac ggaatgtcgt 60
cccagtgggg cgctcccaac gacggctggg gctcgcgcta cggcggcaic agctccgcca 120
gcgactgtct gtccctcccc agcgccctcc aggc 154

<210> 94

<211> 154

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 94

ggggggatcc tgcgtttact tgcgcgagca tccggictta gcggltatci ccttggggca 60
ggltaccctc ttgtaggtca tggacgggtt gtcggcgctc tgaaccagt tgaagcgcca 120
cttgcagccg gcctggaggg cgctggggag ggac 154

<210> 95

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 95

ggggagctca ccttcaccct caccagcggt gctggcaaga agatggtcgt ccaggtcacc 60
aacactggcg gtgacctgg cagctcgacc ggtgccact tcgatctcca gatgcc 117

<210> 96

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 96

ggggggatcc tgcgtttact tgcgcgagca tc 32

<210> 97

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 97

tcagcgggtgg cgctagcggc aac

23

<210> 98

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 98

ctaattggcag cggcagcgaa acc

23

<210> 99

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 99

ccggtgcca cttcgatcic cag

23

<210> 100

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 100

tctttccgcc gcactgtccg tag

23

<210> 101

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 101

acgacaacca gccatgggct gtc

23

<210> 102

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 102

tcicgaatga ctaclacagc cag

23

<210> 103

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 103

cccactggga cgagcatccg ttg

23

<210> 104

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 104

cgagctgctc gattggacg gag

23

<210> 105

<211> 16

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 105

Ala Glu Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn

1

5

10

15

<210> 106

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 106

gactgaccgg tgttcatcc

19

<210> 107

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 107

ctcggttgic atagatgtgg

20

<210> 108

<211> 27

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial-Sequence:primer

cccacagaag ggatcca tga tggtcgc

27

<211> 29

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence:primer

gcgaattcat gaagttcacc gttgctatt

29

<211> 28

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence:primer

gcgaattcctt accttctttc gcaaccttg

28

72/73

<210> 111

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 111

cttgggtgctg ccagcggttac cag

23

<210> 112

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 112

gcggatccat gaagttctcc atcatcg

27

<210> 113

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 113

gcggatcctt acttgcgctc gcaacca